Highlighted Articles

[Quantifying and predicting responses to a West Coast salmon fishery closure](#)
Ecological Applications (4.093)

[Can vessel buybacks pay off: An evaluation of an industry funded fishing vessel buyback](#)
Marine Policy (2.610)

Cross Line Office Articles

[Genetic assignment to stock of stranded common bottlenose dolphins (*Tursiops truncatus*) in southeastern Louisiana after the Deepwater Horizon oil spill](#)
Endangered Species Research (1.325)

Additional Articles
NOS Publications
[Nautilus samples 2016: New techniques and partnerships](#)
Oceanography (2.986)

[Assigning stranded bottlenose dolphins to stock using stable isotope ratios following the deepwater horizon oil spill](#)
Endangered Species Research (1.325)

NMFS Publications
[The robustness of Brownie Tag return models to complex spatiotemporal dynamics evaluated through simulation analysis](#)
Canadian Journal of Fisheries and Aquatic Sciences (2.437)

[Wideband (15-260 kHz) acoustic volume backscattering spectra of northern krill (*Meganyctiphanes norvegica*) and butterfish (*Peprilus triacanthus*)](#)
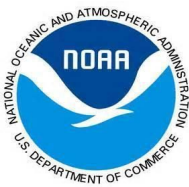
ICES Journal of Marine Science (2.626)

[Envisioning, quantifying, and managing thermal regimes on river networks](#)

Bioscience (4.294)

[Estimating partial compensation to bridge between neutral and niche theory in spatio-temporal community dynamics](#)

Ecology (4.733)

[Habitat-based density models for three cetacean species off Southern California illustrate pronounced seasonal differences](#)

Frontiers in Marine Science (0.72)

[Estimating fish abundance at spawning aggregations from courtship sound levels](#)

Scientific Reports (5.525)

[Effects of clam dredging on benthic ecology of two cultivated northern quahog beds with different harvest histories and sediment grain sizes](#)

Aquaculture International (1.037)

[Genetic assignment with isotopes and habitat suitability (GAIAH), a migratory bird case study](#)

Methods in Ecology and Evolution (6.554)

[Ontogenetic spatial distributions of red grouper (*Epinephelus morio*) and gag grouper (*Mycteroperca microlepis*) in the U.S. Gulf of Mexico](#)

Fisheries Research (1.903)

[Broadband classification and statistics of long-range mid-frequency sonar measurements of aggregations of fish](#)

Journal of the Acoustical Society of America (1.572)
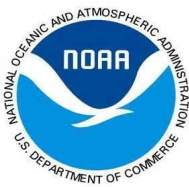
[Population, habitat, and marine location effects on early marine survival and migration behavior of Puget Sound steelhead smolts](#)
Ecosphere (2.287)

[Defining ecosystem thresholds for human activities and environmental pressures in the California Current](#)
Ecosphere (2.287)

[Ecosystem modeling in the Gulf of Mexico: Current status and future needs to address ecosystem-based fisheries management and restoration activities](#)
Reviews in Fish Biology and Fisheries (3.222)

[Advances in the application of genetics in marine turtle biology & conservation](#)
Frontiers in Marine Science, section Marine Conservation and Sustainability

[Buybacks with costly participation](#)
Journal of Environmental Economics and Management (2.197)

[Integrated ecological-economic fisheries models evaluation, review and challenges for implementation](#)
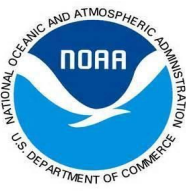Fish and Fisheries (8.258)

[Genetic sexing of pinnipeds: A real-time, single step qPCR technique](#)
Conservation Genetics Resources (0.446)

OAR Publications
[Real-time detection of tsunami ionospheric disturbances with a stand-alone GNSS receiver: A preliminary feasibility demonstration](#)
Scientific Reports (5.228)

HIGHLIGHTED ARTICLES

Quantifying and predicting responses to a West Coast salmon fishery closure
Ecological Applications (4.093)
K. Richerson, **D. S. Holland (NMFS/NWFSC)**

- The analysis suggests the salmon fleet showed little ability to adapt to previous salmon closures by increasing fishing in other fisheries in order to offset lost revenue.
- This means there is probably limited knock-on effects on other fisheries, but also limited ability to cope with variation in landings.

As anthropogenic changes interact with natural climate cycles, the variability of marine ecosystems is likely to increase. This variability influences the behavior of fishermen, which can affect the profitability and sustainability of stocks and may have wider economic and ecological effects. We use data from the West Coast salmon troll fishery before, during, and after a large-scale closure to illustrate how changes in resource availability influence the behavior of fishing vessels in heterogeneous ways. We find that vessels were less likely to participate in any kind of fishing during the closure, with >40% of vessels ceasing fishing during the closure and 17% exiting fishing permanently. Vessels that were more dependent on salmon were more likely to cease fishing during the closure, and more diversified vessels were more likely to continue fishing. Vessels that did fish saw on average a ~30% drop in revenue compared to their average revenue in the years before the closure. In spite of a high level of cross-participation across fisheries, we find limited evidence that vessels increased their participation in other fisheries during the closure. At the port level, ports that historically obtained more of their revenue from the salmon troll fleet saw larger relative decreases in their total revenue during the closure, and this effect persisted into 2010. Overall, the closure was associated with a loss of ~$43 million in fishery revenue relative to the five year period before the closure. Based on our models and the composition of the current fleet, we predict that a potential closure in the near future would have similar or greater impact, suggesting that a closure would cause another economic disaster.
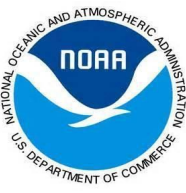
However, our results suggest that effects on fisheries linked by cross-participation are likely to be low.
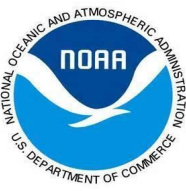
Acceptance date: May 7, 2017

Can vessel buybacks pay off: An evaluation of an industry funded fishing vessel buyback

Marine Policy (2.610)

D. S. Holland, E. Steiner (NMFS/NWFSC), A. Warlick

- The study suggests that the additional quota shares that accrued to groundfish trawl individual fishing quota owners as a result of the buyback are generating sufficient profit to cover the buyback repayment costs.
- The industry has argued those costs are too high and want new terms on the repayment loan.

Fishing vessel and permit buyback programs have been implemented to reduce excess capacity and improve profitability in a number of fisheries around the world. These programs are generally publicly funded, but in a few cases they have been financed by loans to be paid back by the remaining fleet. In 2003 a buyback permanently removed 91 vessels and 239 fishing permits from the Pacific groundfish trawl fishery and associated corollary fisheries of Dungeness crab and pink shrimp. The buyback was financed with $10 million in public funding and a $36 million loan to be repaid over 30 years with fees on landings. In the same year a control date was set for an individual fishing quota (IFQ) program in the groundfish trawl fishery. When the IFQ was implemented in 2011, the permit owners that had remained in the fishery after the buyback were allocated the quota shares that would otherwise have been issued to the permits bought back in 2003. We use estimates of annual net revenue based on comprehensive cost-earnings data, and also estimates of quota lease value, to provide alternative estimates of the annual profits generated by the quota that would have been allocated to the retired permits and compare those values to the cost of servicing the buyback loan. The results provide evidence that a buyback program, when implemented in conjunction with an IFQ, can enable a sustained increase in profitability sufficient to justify the cost of the buyback and provide a means for the industry to finance

consolidation.

Publication date: May 4, 2017

Available online:

http://www.sciencedirect.com/science/article/pii/S0308597X16305711

Cross Line Office Articles

*Genetic assignment to stock of stranded common bottlenose dolphins (*Tursiops truncatus*) in southeastern Louisiana after the Deepwater Horizon oil spill*
Endangered Species Research (1.325)
P. E. Rosel (NMFS/SEFSC), L. A. Wilcox (NMFS/SEFSC), C. Sinclair (NMFS/SEFSC), T. R. Speakman (NOS/NCCOS), MC Tumlin, **J. A. Litz (NMFS/SEFSC), ES Zolman (NOS/NCCOS)**

- Many of the bottlenose dolphins recovered stranded in southeastern Louisiana during, and in the wake of the Deepwater Horizon disaster, originated from the Barataria Bay Estuarine System stock rather than the larger Western Coastal Stock.
- Impacts, from natural or anthropogenic causes, to distinct stocks of bottlenose dolphins can be more accurately modeled by determining the source stock of stranded dolphins.

Degradation of marine ecosystems is an increasing problem and extends beyond nearshore coastal waters with significant human development. However, measuring ecosystem damage and decreased ecosystem function can be difficult. Marine mammals have often been recommended as indicators for evaluating ecosystem health. Between 2010 and the present, a significant cetacean unusual mortality event has occurred across the northern Gulf of Mexico where multiple demographically independent populations of common bottlenose dolphins occur adjacent to one another. Some populations are fairly small and restricted to small habitat areas, while other populations have higher abundances and cover broader geographic ranges. An integral component to determining the impact of this event on these populations is identifying what percentage of each population the stranded animals comprise. We applied genetic assignment test methods to stranded
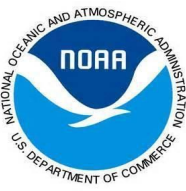
dolphins from southeastern Louisiana to determine the proportion of dead dolphins that came from the local estuarine population versus the population found in adjacent coastal waters. Forty-one microsatellite loci were genotyped in 156 live dolphins sampled to represent the two potential stocks of origin and in 131 dead stranded dolphins of unknown origin. Both classical assignment tests and genetic stock identification methods indicated that approximately 6-7% of the sampled stranded dolphins originated from the Western Coastal Stock and the remainder from the smaller, estuarine stock in Barataria Bay, Louisiana.
Publication date: January 2017
Available online: http://www.int-res.com/abstracts/esr/v33/p221-234/

NOS Publications
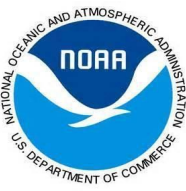
Nautilus samples 2016: New techniques and partnerships
Oceanography (2.986)
N. Raineault, J. Marlow, **M. Everett**, **P. Etnoyer (NOS/NCCOS)**, M. Cormier, V. Knutson, G. Giribet

- This was the first exploration of Arguello Canyon off Southern California. Surveys revealed abundant deep-sea corals near 1500 m depth, and collected a number of new species.
- The Canyon is part of a proposed Chumash Heritage National Marine Sanctuary.
- These expeditions pioneered an emergency technology called "environmental DNA" (eDNA). This technique involves collecting samples of water that contain the DNA of organisms in the environment and can be used to ascertain the presence of certain species, species distribution, population size, and population dynamics, among other variables. It is less invasive and potentially more accurate than directly sampling individuals within populations.
- The live coral sampling and eDNA sampling efforts were very successful. Samples were collected alive and transported to NCCOS Charleston for husbandry in cold-water aquaria.

In 2016, *E/V Nautilus* and the *ROV Hercules* collected 549 geological, biological, and water samples (2,022 subsamples) to characterize several[1] [2] US West Coast national marine sanctuaries, the Cascadia margin, and offshore southern California. Most samples are archived at partner repositories: geological samples to the Marine Geological Samples Lab at the University of Rhode Island and biological samples to Harvard University's Museum of Comparative Zoology. During this field season, we experimented with new sampling methods to improve exploration efficiency and robustness. NOAA researchers successfully collected live samples of deep-water corals for laboratory experiments. Researchers pioneered a new emerging technology called "environmental DNA" also and conducted a series of short ROV transects for benthic habitat characterization.
Publication date: 3/30/2017
Available online:
https://www.researchgate.net/publication/315995304_Nautilus_Samples_2016_New_Techniques_and_Partnerships

Assigning stranded bottlenose dolphins to stock using stable isotope ratios following the deepwater horizon oil spill
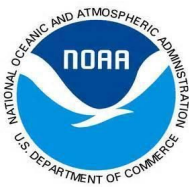Endangered Species Research (1.325)
A. A. Hohn, L. Thomas, R. H. Carmichael, **J. Litz**, C. Clemons-Chevis, S. F. Shippee, **C. Sinclair**, S. Smith, **T. R. Speakman**, M. C. Tumlin, **E. S. Zolman (NOS/NCCOS)**

- Stable isotope (SI) ratios were successfully used to differentiate geographical groups of bottlenose dolphins in the northern Gulf of Mexico.
- On a broader scale SI ratios may prove useful in determining the source habitat of stranded dolphins increasing the utility of data collected from strandings.

The potential for stranded dolphins to serve as a tool for monitoring free-ranging populations would be enhanced if stock (demographically independent populations) were known. We used stable isotopes of carbon, nitrogen and sulfur from skin to assign stranded common bottlenose dolphins (*Tursiops truncatus*) to habitat, as a proxy for stock, from Louisiana through western Florida following the

Deepwater Horizon oil spill. Model results from biopsy samples collected from dolphins from known habitats (n = 205) resulted in an 80.5% probability of correct assignment. These results were applied to data from stranded dolphins (n = 217), resulting in predicted assignment probabilities of 0.473, 0.172, and 0.355 to Estuarine, Barrier Island (BI), and Coastal stocks, respectively. Differences were found west and east of the Mississippi River, with more Coastal dolphins stranding in western Louisiana and more Estuarine dolphins stranding in Mississippi. Two estuarine groups were identified east of the Mississippi River; one associated with estuaries in Mississippi and Alabama and the other associated with estuaries in western Florida. $\delta15N$ values were higher in stranded samples for both Estuarine and Barrier Island stocks, potentially indicating nutritional stress. The high probability of correct assignment of the biopsy samples indicates predictable variation in stable isotopes and fidelity to habitat. The power of $\delta34S$ to discriminate habitats based on salinity was essential. Stable isotopes may provide guidance regarding where additional testing is warranted to confirm demographic independence and aid in determining the source habitat of stranded dolphins, increasing the value of biological data collected from strandings.
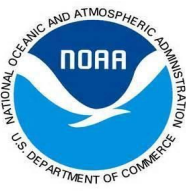Publication date: January 31, 2017
Available online: http://www.int-res.com/articles/esr2017/33/n033p235.pdf

NMFS Publications

The robustness of Brownie Tag return models to complex spatiotemporal dynamics evaluated through simulation analysis
Canadian Journal of Fisheries and Aquatic Sciences
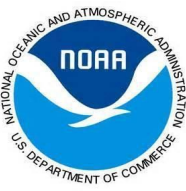**M. V. Lauretta** and **D.R. Goethel (NMFS/SEFSC)**
- Proper experimental design of tagging studies is critical for obtaining reliable parameter estimates with appropriate levels of uncertainty. By simulation testing the experimental design prior to the implementation of the tagging study, it is possible to determine more cost effective release programs (i.e. timing, spatial extent, and number of tag releases).

- A diverse and flexible toolset was created and made available online for testing complex tagging study designs and evaluating the expected benefits in terms of biological parameter and fishing mortality estimation. Simulation testing results indicated that migration rates can be accurately estimated from the conventional tagging program, the need for external information on tag reporting to acquire unbiased estimates of fishing mortality for tropical tunas, and the benefits of genetic tagging of bluefin tuna to improve tagging study outputs.

- By continually refining and applying our spatiotemporal tagging simulator, a better accounting of the potential limitations and sensitivities of tagging models can be explored, and more robust advice on study design can be provided to the funding agencies that implement tagging programs.

The development of a reliable tagging program requires simulation testing the experimental design. However, the potential for model misspecification, particularly in the underlying spatiotemporal dynamics, is often ignored. A continuous time, spatially-explicit, age-structured, capture-recapture operating model was developed to better emulate real-world population dynamics typically overlooked in spatially-aggregated or discrete time tagging models. Various spatiotemporal model parametrizations, including case studies with Atlantic bluefin and yellowfin tunas, were explored to evaluate the bias associated with Brownie tag return estimation models. Simulations demonstrated that accounting for connectivity was essential for obtaining unbiased parameter estimates, and that migration rates could be reliably estimated without the correlation associated with other parameters (e.g., between tag reporting and mortality). Mortality parameter estimates were particularly sensitive to the temporal dynamics of the tagging and fishing seasons, but accounting for the seasonality in tag releases and fishery recaptures allowed for relatively unbiased estimation. Our results indicate that parameter bias and uncertainty can be severely underestimated when discrete time or spatially-aggregated operating models are used to determine optimal experimental design of tagging studies.

Acceptance date: April 27, 2017

*Wideband (15-260 kHz) acoustic volume backscattering spectra of northern krill (*Meganyctiphanes norvegica*) and butterfish (*Peprilus triacanthus*)*
ICES Journal of Marine Science (2.626)
J. M. Jech (NMFS/NEFSC), G. L. Lawson, A. C. Lavery

- Demonstrated consistency of theoretical model with measurements of krill and butterfish at high spectral resolution
- Improved theoretical acoustic model of butterfish, which may be applicable to narrow bandwidth data collected by NEFSC

Measurements of acoustic backscatter made over a wide frequency band have the potential for improved classification relative to traditional narrowband methods, by characterizing more fully the frequency response of scatterers. In January 2014, five wideband transceivers (Simrad EK80 WBTs) and split-beam transducers with nominal center frequencies of 18, 38, 70, 120, and 200 kHz were used to collect acoustic data spanning a nearly continuous 15 to 260 kHz bandwidth. The acoustic samples were from ca. 2 m below the surface to the seabed in an area along the U.S. continental shelf break. Bottom trawls and zooplankton nets were also used to sample scatterers contributing to selected features of the acoustic backscatter. Measurements of frequency-dependent volume backscattering strength (i.e., volume backscattering spectra) from aggregations of euphausiids (mostly Northern krill, Meganyctiphanes norvegica) clearly resolved the transition from Rayleigh to geometric scattering, consistent with modeled backscatter from the type and length of animals sampled with bongo nets. Volume backscattering spectra from aggregations dominated by butterfish (Peprilus triacanthus) revealed a frequency response that was suggestive of superimposed scattering by soft tissue and bone. Backscatter predicted by Kirchhoff ray mode (KRM) models of butterfish corresponded to trends in the measured spectra, supporting the assumption that acoustic scattering by butterfish is dominated by soft tissue and vertebrae. Acceptance date: April 18, 2017

Envisioning, quantifying, and managing thermal regimes on river networks
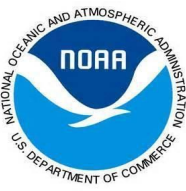Bioscience (4.294)
A. Steel, **T. J. Beechie**, C. E. Torgersen, **A. H. Fullerton (NMFS/NWFSC)**
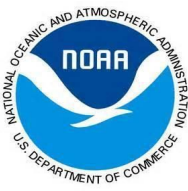
- Advances in data collection and quantitative modeling are refining our vision of the thermal landscape of rivers and ecological responses.
- New science suggests the biological importance of thermal variability and how humans are altering the spatio-temporal complexity of thermal landscapes.
- We synthesize needs and opportunities in riverine management and science based on the emerging understanding of variation in thermal landscapes over time and space.

Water temperatures fluctuate in time and over space, creating diverse thermal regimes on river networks. Temporal variability in these thermal landscapes has important biological and ecological consequences because of nonlinearities in physiological reactions; spatial diversity in thermal landscapes provides aquatic organisms with options to maximize growth and survival. Yet, human activities including climate change threaten to alter dynamics of riverine thermal regimes. New data and tools can identify particular facets of the thermal landscape that represent ecological and management concerns and that are linked to human actions. The emerging complexity of thermal landscapes demands innovations in communication; opens the door to exciting research opportunities on human impacts to and biological consequences of thermal variability; suggests improvements in monitoring programs to better capture empirical patterns; provides a framework for suites of actions to restore and protect the natural processes that drive thermal complexity; and indicates opportunities for better managing thermal landscapes.

Estimating partial compensation to bridge between neutral and niche theory in spatio-temporal community dynamics

Ecology (4.733)

J. T. Thorson (NMFS/NWFSC), S. Munch, and D. Swain

- We develop a spatio-temporal model for density of multiple species, and show that we can accurately estimate interactions, as well as community axes that are not regulated.
- Application to the Gulf of St. Lawrence shows little regulation for recovering grey seals that consume exploited fish species.

Niche-based approaches to community analysis often involve estimating a matrix of pairwise interactions among species (the "community matrix"), but this task becomes infeasible using observational data as the number of modeled species increases. As an alternative, neutral theories achieve parsimony by assuming that species within a trophic level are exchangeable, but generally cannot incorporate stabilizing interactions even when they are evident in field data. Finally, both regulated (niche) and unregulated (neutral) approaches have rarely been fitted directly to survey data using spatiotemporal statistical methods. We therefore propose a spatiotemporal and model-based approach to estimate community dynamics that are partially regulated. Specifically, we start with a neutral spatiotemporal model where all species follow ecological drift, which precludes estimating pairwise interactions. We then add regulatory relations until model selection favors stopping, where the "rank" of the interaction matrix may range from zero to the number of species. A simulation experiment shows that model selection can accurately identify the rank of the interaction matrix, and that the identified spatiotemporal model can estimate the magnitude of species interactions. A 40-yr case study for the Gulf of St. Lawrence marine community shows that recovering grey seals have an unregulated and negative relationship with demersal fishes. We therefore conclude that partial regulation is a plausible approximation to community dynamics using field data and hypothesize that estimating partial regulation will be expedient in future analyses of spatiotemporal community dynamics given limited field data. We conclude by recommending ongoing
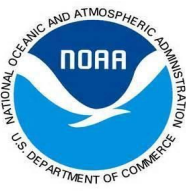
research to add explicit models for movement, so that meta-community theory can be confronted with data in a spatiotemporal statistical framework.
Publication date: May 3, 2017

Habitat-based density models for three cetacean species off Southern California illustrate pronounced seasonal differences
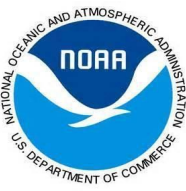Frontiers in Marine Science (0.72)
E. A. Becker, K. A. Forney, B. J. Thayre, A. J. Debich, G. S. Campbell, K. Whitaker, A. B. Douglas, **A. Gilles (NMFS/SWFSC)**, R. Hoopes, and J. A. Hildebrand

- This paper presents the first spatially-explicit habitat-based density models for three cetacean species for winter/spring.
- The resulting model-based cetacean densities were compared to similar summer/fall models, illustrating seasonal changes in distribution for all three species.
- Model results allow for the seasonal assessment of potential anthropogenic impacts.

Managing marine species effectively requires spatially and temporally explicit knowledge of their density and distribution. Habitat-based density models, a type of species distribution model (SDM) that uses habitat covariates to estimate species density and distribution patterns, are increasingly used for marine management and conservation because they provide a tool for assessing potential impacts (e.g., from fishery bycatch, ship strikes, anthropogenic sound) over a variety of spatial and temporal scales. The abundance and distribution of many pelagic species exhibit substantial seasonal variability, highlighting the importance of predicting density specific to the season of interest. This is particularly true in dynamic regions like the California Current, where significant seasonal shifts in cetacean distribution have been documented at coarse scales. Finer scale (10 km) habitat-based density models were previously developed for many cetacean species occurring in this region, but most models were limited to summer/fall. The objectives of our study were two-fold: 1) develop spatially-explicit density estimates for winter/spring to support management applications, and 2) compare model-predicted density and

distribution patterns to previously developed summer/fall model results in the context of species ecology. We used a well-established Generalized Additive Modeling framework to develop cetacean SDMs based on 20 California Cooperative Oceanic Fisheries Investigations (CalCOFI) shipboard surveys conducted during winter and spring between 2005 and 2015. Models were fit for short-beaked common dolphin (*Delphinus delphis delphis*), Dall's porpoise (*Phocoenoides dalli*), and humpback whale (*Megaptera novaeangliae*). Model performance was evaluated based on a variety of established metrics, including the percentage of explained deviance, ratios of observed to predicted density, and visual inspection of predicted and observed distributions. Final models were used to produce spatial grids of average species density and spatially-explicit measures of uncertainty. Results provide the first fine scale (10 km) density predictions for these species during the cool seasons and reveal distribution patterns that are markedly different from summer/fall, thus providing novel insights into species ecology and quantitative data for the seasonal assessment of potential anthropogenic impacts.

Publication date: May 11, 2017

Available online:

http://journal.frontiersin.org/article/10.3389/fmars.2017.00121/full
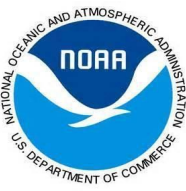

Estimating fish abundance at spawning aggregations from courtship sound levels
Scientific Reports (5.525)
T. J. Rowell, **D. A. Demer**, O. Aburto-Oropeza, J. J. Cota-Nieto, **J. R. Hyde (NMFS/SWFSC)** and B. E. Erisman

- Sound intensity in the area of spawning aggregations may relate to the densities of sound producing fish as estimated from tracked echoes.
- With a validated empirical model of sound intensity versus fish density, passive acoustic sampling may be used to monitor the densities of spawning aggregations of sound producing fish.

Sound produced by fish spawning aggregations (FSAs) permits the use of passive acoustic methods to identify the timing and location of spawning. However, difficulties in relating sound levels to abundance have impeded the use of passive

acoustics to conduct quantitative assessments of biomass. Here we show that models of measured fish sound production versus independently measured fish density can be generated to estimate abundance and biomass from sound levels at FSAs. We compared sound levels produced by spawning Gulf Corvina (Cynoscion othonopterus) with simultaneous measurements of density from active acoustic surveys in the Colorado River Delta, Mexico. During the formation of FSAs, we estimated peak abundance at 1.53 to 1.55 million fish, which equated to a biomass of 2,133 to 2,145 metric tons. Sound levels ranged from 0.02 to 12,738 Pa^2, with larger measurements observed on outgoing tides. The relationship between sound levels and densities was variable across the duration of surveys but stabilized during the peak spawning period after high tide to produce a linear relationship. Our results support the use of active acoustic methods to estimate density, abundance, and biomass of fish at FSAs; using appropriately scaled empirical relationships, sound levels can be used to infer these estimates.
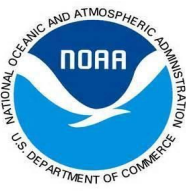Publication date: May 11, 2017

Effects of clam dredging on benthic ecology of two cultivated northern quahog beds with different harvest histories and sediment grain sizes
Aquaculture International (1.037)
R. Mercaldo-Allen, S. Meseck, R. Goldberg, P. Clark, C. Kuropat, and **J. M. Rose (NMFS/NEFSC)**

- Enhances understanding of how the interval between clam dredging events, or harvest history, may influence benthic ecology and response of communities to further dredging.
- Harvest frequency and/or sediment size may explain differences in benthic assemblages between areas with different dredging histories, while dredging had no measurable effect on sediment chemistry.

In Connecticut, cultivation of the northern quahog, or hard clam, Mercenaria mercenaria L., relies on hydraulic dredging. After harvesting, leased shellfish beds remain fallow for varying durations to facilitate natural reseeding and to allow small clams to reach harvestable size. The interval between dredging events, or harvest history, may influence benthic ecology and response of communities to

further dredging. Two clam beds with different harvest histories, located near Milford, Connecticut, were studied from July through October 2012. These leased beds, fallow for 3- and 8-years respectively, were subdivided into two plots. One plot on each bed was commercially harvested in July while the other remained not dredged. Sediment sampling was conducted on alternate weeks using Smith MacIntyre grabs and sediment cores to compare ecology of benthic communities and chemistry of marine sediments on newly dredged and not dredged plots within leases. Main effects of lease (harvest history), dredging treatment (dredged versus not dredged plots), mean sediment phi size (φ) and season (sampling date) significantly affected benthic community structure. Newly settled bivalves, including early successional pioneer species, occurred in high abundance on 3-year beds. Diversity, evenness and number of species was high on the 8-year beds, while abundance of individuals was low, more typical of later successional equilibrium communities. Differences among a subset of species on the 8-year beds were observed between dredged and not dredged plots while no community differences were observed between dredging treatments on 3-year beds. Significantly more individuals were observed on dredged versus not dredged plots on the 8-year beds only. Our results suggest that harvest frequency and/or sediment φ size may explain differences in benthic assemblages between leased areas with different dredging histories, while dredging had no measurable effect on sediment chemistry.
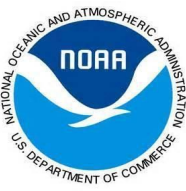
Acceptance date: May 2017

Genetic assignment with isotopes and habitat suitability (GAIAH), a migratory bird case study
Methods in Ecology and Evolution (6.554)
K. C. Ruegg, **E. C. Anderson (NMFS/SWFSC)**, R. J. Harrigan, K. L. Paxton, J. F. Kelly, F. Moore, T. B. Smith

- Breeding locations of migrating organisms can be estimated more accurately.
- Methods developed for tracking migratory salmon are useful for birds.

- Genetic markers have the potential to be considerably more powerful than stable isotopes for tracking migratory organisms.

1. Identifying migratory connections across the annual cycle is important for studies of migrant ecology, evolution, and conservation. While recent studies have demonstrated the utility of high-resolution SNP-based genetic markers for identifying population-specific migratory patterns, the accuracy of this approach relative to other intrinsic tagging techniques has not yet been assessed.

2. Here, using a straightforward application of Bayes' Rule, we develop a method for combining inferences from high-resolution genetic markers, stable isotopes, and habitat suitability models, to spatially infer the breeding origin of migrants captured anywhere along their migratory pathway. Using leave-one-out cross validation, we compare the accuracy of this combined approach with the accuracy attained using each source of data independently.

3. Our results indicate that when each method is considered in isolation, the accuracy of genetic assignments far exceeded that of assignments based on stable isotopes or habitat suitability models. However, our joint assignment method consistently resulted in small, but informative increases in accuracy and did help to correct misassignments based on genetic data alone. We demonstrate the utility of the combined method by identifying previously undetectable patterns in the timing of migration in a North American migratory songbird, the Wilson's warbler.

4. Overall, our results support the idea that while genetic data provides the most accurate method for tracking animals using intrinsic markers, when each method is considered independently, there is value in combining all three methods. The resulting methods are provided as part of a new computationally-efficient R-package, \sw{gaiah}, allowing broad application of our statistical framework to other migratory animal systems.
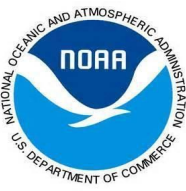
Publication date: May 3, 2017

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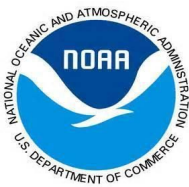
http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12800/full

*Ontogenetic spatial distributions of red grouper (*Epinephelus morio*) and gag grouper (*Mycteroperca microlepis*) in the U.S. Gulf of Mexico*
Fisheries Research (1.903)
A. Grüss, **J. T. Thorson**, **S. R. Sagarese**, E. A. Babcock, **M. Karnauskas**, **J. F. Walter (NMFS/SEFSC)**, M. Drexler

- Predictions of spatial distribution concur with understanding of grouper distributions in the Gulf of Mexico.
- Our approach identified potential spawning grounds for gag grouper.
- Our study will help improve the maps fed into ecosystem models of the Gulf of Mexico.

Mapping the spatial distributions of fish populations is an integral component of ecosystem-based fisheries management (EBFM). Particularly for red grouper (*Epinephelus morio*) and gag grouper ("gag"; *Mycteroperca microlepis*), two economically important species, the lack of mapping due to data limitations (i.e., inconsistent capture in research surveys) has left a critical gap in the science needed to assess how ecosystem processes and EBFM measures in the Gulf of Mexico (GOM) impact their population dynamics. We combined multiple fisheries-dependent and fisheries-independent data sources to map the long-term spatial distributions of older juveniles and adults of red and gag groupers in the U.S. GOM, using spatio-temporal binomial generalized linear mixed models (GLMMs). Spatio-temporal binomial GLMMs rely on the idea that probability of encounter at a given site is more similar to probability of encounter at nearby sites than to probability of encounter at geographically remote locations; this tenet allows one to estimate a smoothed surface depicting how probability of encounter varies spatially. Our spatio-temporal binomial GLMMs do not integrate environmental covariates, yet they account for the effects of year and research survey. The distribution maps produced from the predictions of the spatio-temporal binomial GLMMs aligned with the current understanding of the long-term ontogenetic spatial distributions of red and gag groupers in the U.S. GOM. Red grouper was predicted to be encountered throughout the West Florida Shelf (WFS),

primarily at depths ranging from 20 to 60 m. Both older juvenile and adult female gags were predicted to be encountered from Apalachicola, Florida, to the region northwest of Tampa, Florida, along the 20 m depth contour, especially in Apalachee Bay. The probability of encounter of adult female gag was also high in the Florida Middle Grounds and in deeper (> 40 m) areas of the WFS. The probability of encounter of adult male gag was highest along the edge of the WFS, both inside recognized spawning grounds (including the Madison-Swanson marine protected area) and outside, i.e., below 27°N (including Pulley Ridge). The distribution maps produced are valuable for understanding the ecology of grouper species and can be used as a basis for further analyses. Our spatio-temporal binomial GLMM framework will serve many important EBFM projects, including the construction of reliable distribution maps in bulk for spatially explicit ecosystem models of the GOM, which will improve spatial distributions and species spatial overlaps in spatially explicit ecosystem models and, therefore, the trophic interactions predicted by these models.

Publication date: April 25, 2017

Available online:

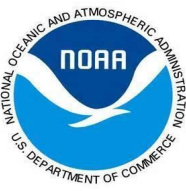http://www.sciencedirect.com/science/article/pii/S016578361730111X

Broadband classification and statistics of long-range mid-frequency sonar measurements of aggregations of fish
Journal of the Acoustical Society of America (1.572)
B. Jones, T. K. Stanton, J. A. Colosi, R. C. Gauss, J. M. Fialkowski, **J. M. Jech (NMFS/NEFSC)**

- Demonstrated utility of long-range sonar for detecting fish schools
- Demonstrated consistency between theoretical models of acoustic scattering and measurements of fish schools

Scattering from fish can constitute a significant portion of the high-amplitude echoes in the case of a horizontal-looking sonar system operating at mid-frequencies (1--10 kHz). In littoral environments, reverberation from fish with resonant gas-filled swimbladders can dominate bottom and surface reverberation and add spatio-temporal variability to an already complex acoustic record.

Measurements of sparsely distributed, spatially compact fish aggregations were conducted in the Gulf of Maine using a long-range, broadband sonar with continuous coverage over the frequency band of 1.5–5 kHz. Concurrent downward-looking, multi-frequency echosounder measurements (18, 38, and 120 kHz) and net samples of fish were used in conjunction with physics-based acoustic models to classify and statistically characterize the long-range fish echoes. A significant number of echoes at least 15 decibels above background levels were observed in the long-range data. These echoes were classified in the frequency domain as swimbladder resonances from mixed assemblages of swimbladder-bearing fish. The echo magnitudes of these aggregations of fish have highly non-Rayleigh distributions. The probability density functions of the echoes are accurately predicted by a computationally efficient, physics-based model that accounts for beam-pattern and waveguide effects as well as the scattering response of aggregations of fish.
Acceptance date: May 2, 2017

Population, habitat, and marine location effects on early marine survival and migration behavior of Puget Sound steelhead smolts
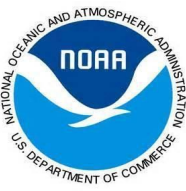Ecosphere (2.287)
M. E. Moore, B. A. Berejikian (NMFS/NWFSC)
  ● This study investigated the influence of population, freshwater environment, and marine conditions on the survival of two Puget Sound steelhead trout populations.
  ● The study suggests early marine survival patterns are driven by marine conditions and not by effects of population or freshwater rearing conditions.
Steelhead trout (*Onchorhynchus mykiss*) smolts suffer high mortality rates during their rapid migration through the Salish Sea. Among-population variability in mortality rates may reflect i) genetic fitness variation among populations, ii) freshwater environmental effects on fish condition, or iii) differences in local marine conditions upon seawater entry. A reciprocal transplant experiment was conducted to separate the influence of freshwater effects (combined effects of population and freshwater environment) from effects of local marine conditions on

survival of two Puget Sound steelhead populations. Steelhead smolts from the Green River in Central Puget Sound (urbanized and hatchery-influenced) and the Nisqually River in South Puget Sound (less urbanized; no hatchery influence) were tagged with acoustic telemetry transmitters and released back into their natal river or transported and released into the other river. Population-of-origin had little influence on probability of surviving the migration through Puget Sound. However, smolts released into the Green River had higher survival through Puget Sound (17%) than smolts released into the Nisqually River (6%); the extra 60-km migration segment for the Nisqually-released fish accounted for most of the difference between the two release locations. Neither fork length nor translocation influenced survival, though release date did affect survival of Nisqually population smolts regardless of their release location. Residence time and behavior in the two estuaries were similar, and no effects of population-of-origin or release date were evident. Marine travel rates also did not differ between populations, release dates, or release locations. This study indicates that mortality occurring in the Salish Sea is likely driven by processes in inland marine environments, more so than latent effects of freshwater environments on fish condition.
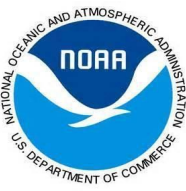
Acceptance date: April 20, 2017

Defining ecosystem thresholds for human activities and environmental pressures in the California Current

Ecosphere (2.287)

J. F. Samhouri (NMFS/NWFSC), K. S. Andrews (NMFS/NWFSC), G. Fay, **C. J. Harvey (NMFS/NWFSC), E. L. Hazen (NMFS/SWFSC),** S. Hennessey, **K. K. Holsman (NMFS/NWFSC), M. E. Hunsicker (NMFS/NWFSC)**, S. I. Large, K. Marshall, A. C. Stier, J. Tam, **S. Zador (NMFS/AFSC)**
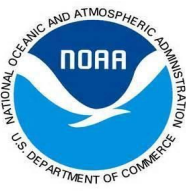
- We developed a framework based on multimodel inference to define ecosystem-based thresholds for human and environmental pressures in the California Current marine ecosystem.
- These analyses identified the existence of threshold responses of five ecosystem states to four environmental and two human pressures.

- This research provides a new way to interpret changes in the intensities of human and environmental pressures as they relate to the ecological integrity of the California Current ecosystem and can be used to make more informed assessments of when and under what conditions intervention, preparation, and mitigation may enhance progress toward ecosystem-based management goals.

The oceans are changing more rapidly than ever before. Unprecedented climatic variability is interacting with unmistakable long-term trends, all against a backdrop of intensifying human activities. What remains unclear, however, is how to evaluate whether conditions have changed enough to provoke major responses of species, habitats, and communities. We developed a framework based on multimodel inference to define ecosystem-based thresholds for human and environmental pressures in the California Current marine ecosystem. To demonstrate how to apply the framework, we used gradient forest and generalized additive model (GAM) analyses to screen for nonlinearities and potential threshold responses of ecosystem states (n=9) across environmental (n=6) and human (n=10) pressures. These analyses identified the existence of threshold responses of five ecosystem states to four environmental and two human pressures. Gradient forest analyses revealed that mean trophic level of the groundfish community, northern (boreal) copepod biomass for both summer and winter, and scavenger biomass had significant thresholds explained by indices of environmental pressures, namely the Pacific Decadal Oscillation ('PDO', during summer and winter months), and a human activity (commercial shipping). The GAMs revealed a significant nonlinearity between a different ecosystem state—California sea lion pup production—and annual variation in summer PDO values. Furthermore, the GAM analysis detected nonlinear relationships between California sea lion pup production and the Northern Oscillation Index during summer; northern copepod biomass during summer and the North Pacific Gyre Oscillation during winter; and, northern copepod biomass during winter and an indicator of human-caused habitat modification. Taken together, our findings provide a new way to interpret changes in the intensities of human and environmental pressures as they relate to the ecological integrity of the California Current ecosystem. These insights can be

used to make more informed assessments of when and under what conditions
intervention, preparation, and mitigation may enhance progress toward
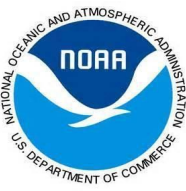ecosystem-based management goals.

*Ecosystem modeling in the Gulf of Mexico: current status and future needs to
address ecosystem-based fisheries management and restoration activities*
Reviews in Fish Biology and Fisheries (3.222)
H. O'Farrell, A. Grüss, **S. R. Sagarese (NMFS/SEFSC)**, E. A. Babcock, K. A.
Rose

- The current status of ecosystem modeling efforts is reviewed for the U.S.
  Gulf of Mexico and whole Gulf of Mexico large marine ecosystem and
  future needs to address ecosystem-based fisheries management and
  restoration in these regions are identified.
- In addition to reviewing the purposes, capabilities, use, and main findings of
  ecosystem models in the Gulf of Mexico, we discuss how
  ecosystem-modeling approaches not currently implemented in the Gulf of
  Mexico may provide useful insights to ecosystem-based fisheries
  management and restoration programs and projects.

Many ecosystem-based fisheries management (EBFM) measures and restoration
projects have been implemented to address the stressors that have negatively
affected the United States (U.S.) Gulf of Mexico (GOM). Ecosystem simulation
models are useful tools for tackling EBFM and restoration questions. Here, we
review the current status of ecosystem modeling efforts for the U.S. GOM and
whole GOM large marine ecosystem and identify future needs to address EBFM
and restoration in these regions. Existing ecosystem models of the GOM are
diverse, ranging from simple conceptual and qualitative models to
biogeochemical-based end-to-end models and coupled and hybrid model platforms.
Many models have focused on understanding the structure and functioning of
GOM ecosystems and the impacts of EBFM measures such as bycatch reduction
strategies and marine protected areas. By contrast, a small number of ecosystem
models have been used specifically to address the other EBFM issues of the GOM

and to assess restoration efforts (e.g., marsh restoration). The demands for EBFM and state and gulf-wide restoration activities will both be increasing in the GOM. Therefore, there is a critical need to better employ and enhance existing ecosystem models of the GOM, and to develop new ecosystem models, to more comprehensively address the different EBFM and restoration needs in the region. We provide suggestions to facilitate this endeavor. The development of consistent libraries of ecosystem models and gap analyses such as ours will help fisheries scientists to effectively tackle specific resource management questions in the different marine regions of the world.
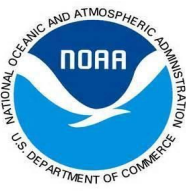
Advances in the application of genetics in marine turtle biology & conservation
Frontiers in Marine Science, section Marine Conservation and Sustainability

L. M. Komoroske, M. P. Jensen, K. Stewart, B. M. Shamblin**, P. H. Dutton (NMFS/SWFSC)**

- Provides overview of the state of the field (including emerging approaches and challenges) to inform marine turtle research and conservation community
- Provides practical guidance for scientists and managers on integrating genetics into biological monitoring programs

Marine turtles migrate across long distances, exhibit complex life histories, and occupy habitats that are difficult to observe. These factors present substantial challenges to understanding fundamental aspects of their biology or assessing human impacts, many of which are important for the effective conservation of these threatened and endangered species. The early development and application of genetic tools made important contributions to understanding marine turtle population and evolutionary biology, such as providing evidence of regional natal homing by breeding adults, establishing connectivity between rookeries and foraging habitats, and determining phylogeography and broad scale stock structure for most marine turtle species. Recent innovations in molecular technologies, statistical methods, and creative application of genetic tools have significantly built upon this knowledge to address key questions in marine turtle biology and

conservation management. Here, we evaluate the latest major advances and potential of marine turtle genetic applications, including improved resolution and large-scale syntheses of population structure, connectivity and phylogeography, estimation of key demographic rates such as age to maturity and operational or breeding sex ratios, insight into reproductive strategies and behavior, and assessment of differential human impacts among populations. We then discuss remaining challenges and emerging capabilities, such as rapid, multiplexed genotyping and investigation of the genomic underpinnings of adaptive variation afforded by high-throughput sequencing technologies.

Buybacks with costly participation

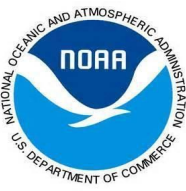J. Holzer, **G. DePiper (NMFS/NEFSC), D. W. Lipton (NMFS/OST)**

- Transaction costs have been directly linked to the success or failure of conservation measures generally, and more recently in the ability of auctions in achieving conservation objectives.
- In the face of transaction costs, lotteries can help bridge the gap between the simplicity of posted offer buybacks and flexibility of auctions in conservation management.
- Even small differentials in transaction costs can erode an auction's efficiency when compared to the lottery.

Posted price offers and first price auctions, along with the multi-unit discriminatory auction extension, are two widely used mechanisms for allocating conservation contracts. The choice between the two typically hinges on the trade-off between the posted price's simplicity and the potential revenue gains of the auction. In this paper we introduce a novel mechanism that attempts to bridge the gap between the performance of posted price offers and auctions. A two-price and lottery schedule combines the simplicity of the former with some of the flexibility of the latter. Using a model that incorporates agents' cognitive and information costs of bidding, we analyze how the ranking of allocative efficiency and cost-effectiveness between the mechanisms varies as the wedge of participation costs increases. When the

number of bidders is endogenously determined by participation costs, bid shading associated with a lack of competition in the auction compromises its cost-effectiveness vis-à-vis the posted price and the lottery schedule. We use data from three recent buybacks for fishing licenses conducted in Maryland to calibrate our model and identify conditions under which the two-price schedule outperforms the other mechanisms.
Publication date: May 4, 2017
Available online:
http://www.sciencedirect.com/science/article/pii/S0095069616300742

Integrated ecological-economic fisheries models evaluation, review and challenges for implementation
Fish and Fisheries (8.258)
R. J. Nielsen, E. Thunberg, **D. S. Holland (NMFS/NWFSC),** J. O. Schmidt, E. A. Fulton, F. Bastardie, and A. E. Punt
- This paper discusses progress in Ecological-Economic models for fisheries and identifies trade-offs between modeling choices (e.g. simplicity, scale, etc.).
- This paper presents a global review and comparative evaluation of a range of models applied to marine fisheries and marine ecosystem resources to identify the characteristics that determine their usefulness, effectiveness and implementation.

Marine ecosystems evolve under many interconnected and area-specific pressures. In order to fulfill society's intensifying and diversifying needs whilst ensuring ecologically sustainable development, more effective marine spatial planning and broader-scope management of marine resources is necessary. Integrated ecological–socioeconomic fisheries models (IESFM) of marine systems are needed to evaluate impacts and sustainability of potential management actions and understand, and anticipate ecological, economic, and social dynamics at a range of scales from local to national and regional. To make these models most effective, it is important to determine how model characteristics and methods of communicating results influence the model implementation, the nature of the
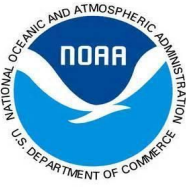
advice that can be provided and the impact on decisions taken by managers. This paper presents a global review and comparative evaluation of 35 IESFM´s applied to marine fisheries and marine ecosystem resources to identify the characteristics that determine their usefulness, effectiveness and implementation. The focus is on fully integrated models that allow for feedbacks between ecological and human processes though not all the models reviewed achieve that.

Acceptance date: May 2, 2017

Genetic sexing of pinnipeds: A real-time, single step qPCR technique
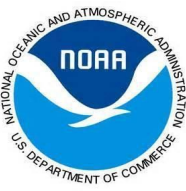Conservation Genetics Resources (0.446)

K. M. Robertson, M. L. Lauf, and **P. A. Morin Robertson (NMFS/SWFSC)**

- The methodology described in this study reduces the cost of running sex determination tests through reduction of labor and supply costs.
- Accurate sex determination of animals is critical to life history and population health studies, specifically aiding in sex ratios, dispersal patterns, behavioral traits and conservation of endangered species.

Existing molecular techniques to determine sex of pinnipeds rely on multiplex PCR amplification and gel electrophoresis, and are consequently expensive, time consuming, insensitive and involve handling hazardous DNA-binding dyes. We developed a qPCR high resolution melt (HRM) assay that involves a single multiplex PCR with dissociation/melting-curve analysis to determine the melting point temperatures (Tm) of two PCR products. Two sets of primers were selected to amplify short regions of the SRY and ZFX/ZFY loci for molecular sex identification. Primers were designed based on alignment of a broad range of pinniped species to maximize applicability for most or all of the 33 species representing 2 complete superfamilies in the sub-order Caniformia. The assay was validated using 15 pinniped species totaling 122 animals of known sex. The co-amplification of short products also demonstrated improved results for sex determination of degraded samples. The use of a single step qPCR saves time and reduces the cost of running sex determination tests through reduction of labor and supply costs. This new technique will generate results more quickly and reliably, aiding in the study of population health and sex-specific dispersal and behavior

patterns.
Publication date: April 29, 2017
Available online: https://link.springer.com/article/10.1007/s12686-017-0759-4

OAR Publications

Real-time detection of tsunami ionospheric disturbances with a stand-alone GNSS receiver:A preliminary feasibility demonstration
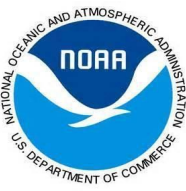Scientific Reports (5.228)
G. Savastano, A. Komjathy, O. Verkhoglyadova, O. Yang, A. Mazzoni, M. Crespi, **Y. Wei (OAR/PMEL)**, and A.J. Mannucci

- Tsunamis can produce gravity waves that propagate up to the ionosphere generating disturbed electron densities in the E and F regions.
- These disturbances can be studied in detail using ionospheric total electron content (TEC) measurements collected by continuously operating ground-based receivers from the Global Navigation Satellite Systems (GNSS)
- The authors present results using a new approach, named VARION (Variometric Approach for Real-Time Ionosphere Observation), and estimate slant TEC (sTEC) variations in a real-time scenario.

It is well known that tsunamis can produce gravity waves that propagate up to the ionosphere generating disturbed electron densities in the E and F regions. These ionospheric disturbances can be studied in detail using ionospheric total electron content (TEC) measurements collected by continuously operating ground-based receivers from the Global Navigation Satellite Systems (GNSS). Here, we present results using a new approach, named VARION (Variometric Approach for Real-Time Ionosphere Observation), and estimate slant TEC (sTEC) variations in a real-time scenario. Using the VARION algorithm we compute TEC variations at 56 GPS receivers in Hawaii as induced by the 2012 Haida Gwaii tsunami event. We observe TEC perturbations with amplitudes of up to 0.25 TEC units and traveling ionospheric perturbations (TIDs) moving away from the earthquake epicenter at an approximate speed of 316 m/s. We perform a wavelet analysis to

analyze localized variations of power in the TEC time series and we find perturbation periods consistent with a tsunami typical deep ocean period. Finally, we present comparisons with the real-time tsunami MOST (Method of Splitting Tsunami) model produced by the NOAA Center for Tsunami Research and we observe variations in TEC that correlate in time and space with the tsunami waves.

Publication date: April 21, 2017

Available online: https://www.nature.com/articles/srep46607#